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## RAW SEQUENCE LISTING

DATE: 01/28/2002

PATENT APPLICATION: US/09/818,247

TIME: 14:33:19

Input Set : A:\UCSF-9-lus.app

Output Set: N:\CRF3\01282002\I818247.raw

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3 <110> APPLICANT: Mostov, Keith E.
4   Chapin, Steven J.
5   Richman-Eisenstat, Janice
6   The Regents of the University of California
8 <120> TITLE OF INVENTION: Ligands Directed to the Non-Secretory Component,
9   Non-Stalk Region of pIgR and Methods of Use Thereof
11 <130> FILE REFERENCE: 18062E-000910US
13 <140> CURRENT APPLICATION NUMBER: US 09/818,247
14 <141> CURRENT FILING DATE: 2001-03-26
16 <150> PRIOR APPLICATION NUMBER: WO PCT/US01/09699
17 <151> PRIOR FILING DATE: 2001-03-26
19 <150> PRIOR APPLICATION NUMBER: US 60/192,197
20 <151> PRIOR FILING DATE: 2000-03-27
22 <150> PRIOR APPLICATION NUMBER: US 60/192,198
23 <151> PRIOR FILING DATE: 2000-03-27
25 <160> NUMBER OF SEQ ID NOS: 26
27 <170> SOFTWARE: PatentIn Ver. 2.1
29 <210> SEQ ID NO: 1
30 <211> LENGTH: 764
31 <212> TYPE: PRT
32 <213> ORGANISM: Homo sapiens
34 <220> FEATURE:
35 <223> OTHER INFORMATION: human polymeric Immunoglobulin receptor (pIgR)
37 <400> SEQUENCE: 1
38 Met Leu Leu Phe Val Leu Thr Cys Leu Leu Ala Val Phe Pro Ala Ile
39   1             5             10             15
41 Ser Thr Lys Ser Pro Ile Phe Gly Pro Glu Glu Val Asn Ser Val Glu
42   20             25             30
44 Gly Asn Ser Val Ser Ile Thr Cys Tyr Tyr Pro Pro Thr Ser Val Asn
45   35             40             45
47 Arg His Thr Arg Lys Tyr Trp Cys Arg Gln Gly Ala Arg Gly Gly Cys
48   50             55             60
50 Ile Thr Leu Ile Ser Ser Glu Gly Tyr Val Ser Ser Lys Tyr Ala Gly
51   65             70             75             80
53 Arg Ala Asn Leu Thr Asn Phe Pro Glu Asn Gly Thr Phe Val Val Asn
54   85             90             95
56 Ile Ala Gln Leu Ser Gln Asp Asp Ser Gly Arg Tyr Lys Cys Gly Leu
57   100            105            110
59 Gly Ile Asn Ser Arg Gly Leu Ser Phe Asp Val Ser Leu Glu Val Ser
60   115            120            125
62 Gln Gly Pro Gly Leu Leu Asn Asp Thr Lys Val Tyr Thr Val Asp Leu
63   130            135            140
65 Gly Arg Thr Val Thr Ile Asn Cys Pro Phe Lys Thr Glu Asn Ala Gln

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66 145          150          155          160
68 Lys Arg Lys Ser Leu Tyr Lys Gln Ile Gly Leu Tyr Pro Val Leu Val
69          165          170          175
71 Ile Asp Ser Ser Gly Tyr Val Asn Pro Asn Tyr Thr Gly Arg Ile Arg
72          180          185          190
74 Leu Asp Ile Gln Gly Thr Gly Gln Leu Leu Phe Ser Val Val Ile Asn
75          195          200          205
77 Gln Leu Arg Leu Ser Asp Ala Gly Gln Tyr Leu Cys Gln Ala Gly Asp
78          210          215          220
80 Asp Ser Asn Ser Asn Lys Lys Asn Ala Asp Leu Gln Val Leu Lys Pro
81 225          230          235          240
83 Glu Pro Glu Leu Val Tyr Glu Asp Leu Arg Gly Ser Val Thr Phe His
84          245          250          255
86 Cys Ala Leu Gly Pro Glu Val Ala Asn Val Ala Lys Phe Leu Cys Arg
87          260          265          270
89 Gln Ser Ser Gly Glu Asn Cys Asp Val Val Val Asn Thr Leu Gly Lys
90          275          280          285
92 Arg Ala Pro Ala Phe Glu Gly Arg Ile Leu Leu Asn Pro Gln Asp Lys
93          290          295          300
95 Asp Gly Ser Phe Ser Val Ile Thr Gly Leu Arg Lys Glu Asp Ala
96 305          310          315          320
98 Gly Arg Tyr Leu Cys Gly Ala His Ser Asp Gly Gln Leu Gln Glu Gly
99          325          330          335
101 Ser Pro Ile Gln Ala Trp Gln Leu Phe Val Asn Glu Glu Ser Thr Ile
102          340          345          350
104 Pro Arg Ser Pro Thr Val Val Lys Gly Val Ala Gly Ser Ser Val Ala
105          355          360          365
107 Val Leu Cys Pro Tyr Asn Arg Lys Glu Ser Lys Ser Ile Lys Tyr Trp
108          370          375          380
110 Cys Leu Trp Glu Gly Ala Gln Asn Gly Arg Cys Pro Leu Leu Val Asp
111 385          390          395          400
113 Ser Glu Gly Trp Val Lys Ala Gln Tyr Glu Gly Arg Leu Ser Leu Leu
114          405          410          415
116 Glu Glu Pro Gly Asn Gly Thr Phe Thr Val Ile Leu Asn Gln Leu Thr
117          420          425          430
119 Ser Arg Asp Ala Gly Phe Tyr Trp Cys Leu Thr Asn Gly Asp Thr Leu
120          435          440          445
122 Trp Arg Thr Thr Val Glu Ile Lys Ile Ile Glu Gly Glu Pro Asn Leu
123          450          455          460
125 Lys Val Pro Gly Asn Val Thr Ala Val Leu Gly Glu Thr Leu Lys Val
126 465          470          475          480
128 Pro Cys His Phe Pro Cys Lys Phe Ser Ser Tyr Glu Lys Tyr Trp Cys
129          485          490          495
131 Lys Trp Asn Asn Thr Gly Cys Gln Ala Leu Pro Ser Gln Asp Glu Gly
132          500          505          510
134 Pro Ser Lys Ala Phe Val Asn Cys Asp Glu Asn Ser Arg Leu Val Ser
135          515          520          525
137 Leu Thr Leu Asn Leu Val Thr Arg Ala Asp Glu Gly Trp Tyr Trp Cys
138          530          535          540

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140 Gly Val Lys Gln Gly His Phe Tyr Gly Glu Thr Ala Ala Val Tyr Val
141 545 550 555 560
143 Ala Val Glu Glu Arg Lys Ala Ala Gly Ser Arg Asp Val Ser Leu Ala
144 565 570 575
146 Lys Ala Asp Ala Ala Pro Asp Glu Lys Val Leu Asp Ser Gly Phe Arg
147 580 585 590
149 Glu Ile Glu Asn Lys Ala Ile Gln Asp Pro Arg Leu Phe Ala Glu Glu
150 595 600 605
152 Lys Ala Val Ala Asp Thr Arg Asp Gln Ala Asp Gly Ser Arg Ala Ser
153 610 615 620
155 Val Asp Ser Gly Ser Ser Glu Glu Gln Gly Gly Ser Ser Arg Ala Leu
156 625 630 635 640
158 Val Ser Thr Leu Val Pro Leu Gly Leu Val Leu Ala Val Gly Ala Val
159 645 650 655
161 Ala Val Gly Val Ala Arg Ala Arg His Arg Lys Asn Val Asp Arg Val
162 660 665 670
164 Ser Ile Arg Ser Tyr Arg Thr Asp Ile Ser Met Ser Asp Phe Glu Asn
165 675 680 685
167 Ser Arg Glu Phe Gly Ala Asn Asp Asn Met Gly Ala Ser Ser Ile Thr
168 690 695 700
170 Gln Glu Thr Ser Leu Gly Lys Glu Glu Phe Val Ala Thr Thr Glu
171 705 710 715 720
173 Ser Thr Thr Glu Thr Lys Glu Pro Lys Lys Ala Lys Arg Ser Ser Lys
174 725 730 735
176 Glu Glu Ala Glu Met Ala Tyr Lys Asp Phe Leu Leu Gln Ser Ser Thr
177 740 745 750
179 Val Ala Ala Glu Ala Gln Asp Gly Pro Gln Glu Ala
180 755 760
183 <210> SEQ ID NO: 2
184 <211> LENGTH: 757
185 <212> TYPE: PRT
186 <213> ORGANISM: Bos taurus
188 <220> FEATURE:
189 <223> OTHER INFORMATION: bovine polymeric immunoglobulin receptor (pIgR)
191 <400> SEQUENCE: 2
192 Met Ser Arg Leu Phe Leu Ala Cys Leu Leu Ala Ile Phe Pro Val Val
193 1 5 10 15
195 Ser Met Lys Ser Pro Ile Phe Gly Pro Glu Glu Val Thr Ser Val Glu
196 20 25 30
198 Gly Arg Ser Val Ser Ile Lys Cys Tyr Tyr Pro Pro Thr Ser Val Asn
199 35 40 45
201 Arg His Thr Arg Lys Tyr Trp Cys Arg Gln Gly Ala Gln Gly Arg Cys
202 50 55 60
204 Thr Thr Leu Ile Ser Ser Glu Gly Tyr Val Ser Asp Asp Tyr Val Gly
205 65 70 75 80
207 Arg Ala Asn Leu Thr Asn Phe Pro Glu Ser Gly Thr Phe Val Val Asp
208 85 90 95
210 Ile Ser His Leu Thr His Lys Asp Ser Gly Arg Tyr Lys Cys Gly Leu
211 100 105 110

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213 Gly Ile Ser Ser Arg Gly Leu Asn Phe Asp Val Ser Leu Glu Val Ser
214      115      120      125
216 Gln Asp Pro Ala Gln Ala Ser His Ala His Val Tyr Thr Val Asp Leu
217      130      135      140
219 Gly Arg Thr Val Thr Ile Asn Cys Pro Phe Thr Arg Ala Asn Ser Glu
220 145      150      155      160
222 Lys Arg Lys Ser Leu Cys Lys Lys Thr Ile Gln Asp Cys Phe Gln Val
223      165      170      175
225 Val Asp Ser Thr Gly Tyr Val Ser Asn Ser Tyr Lys Asp Arg Ala His
226      180      185      190
228 Ile Ser Ile Leu Gly Thr Asn Thr Leu Val Phe Ser Val Val Ile Asn
229      195      200      205
231 Arg Val Lys Leu Ser Asp Ala Gly Met Tyr Val Cys Gln Ala Gly Asp
232      210      215      220
234 Asp Ala Lys Ala Asp Lys Ile Asn Ile Asp Leu Gln Val Leu Glu Pro
235 225      230      235      240
237 Glu Pro Glu Leu Val Tyr Gly Asp Leu Arg Ser Ser Val Thr Phe Asp
238      245      250      255
240 Cys Ser Leu Gly Pro Glu Val Ala Asn Val Pro Lys Phe Leu Cys Gln
241      260      265      270
243 Lys Lys Asn Gly Gly Ala Cys Asn Val Val Ile Asn Thr Leu Gly Lys
244      275      280      285
246 Lys Ala Gln Asp Phe Gln Gly Arg Ile Val Ser Val Pro Lys Asp Asn
247      290      295      300
249 Gly Val Phe Ser Val His Ile Thr Ser Leu Arg Lys Glu Asp Ala Gly
250 305      310      315      320
252 Arg Tyr Val Cys Gly Ala Gln Pro Glu Gly Glu Pro Gln Asp Gly Trp
253      325      330      335
255 Pro Val Gln Ala Trp Gln Leu Phe Val Asn Glu Glu Thr Ala Ile Pro
256      340      345      350
258 Ala Ser Pro Ser Val Val Lys Gly Val Arg Gly Gly Ser Val Thr Val
259      355      360      365
261 Ser Cys Pro Tyr Asn Pro Lys Asp Ala Asn Ser Ala Lys Tyr Trp Cys
262      370      375      380
264 His Trp Glu Glu Ala Gln Asn Gly Arg Cys Pro Arg Leu Val Glu Ser
265 385      390      395      400
267 Arg Gly Leu Ile Lys Glu Gln Tyr Glu Gly Arg Leu Ala Leu Leu Thr
268      405      410      415
270 Glu Pro Gly Asn Gly Thr Tyr Thr Val Ile Leu Asn Gln Leu Thr Asp
271      420      425      430
273 Gln Asp Thr Gly Phe Tyr Trp Cys Val Thr Asp Gly Asp Thr Arg Trp
274      435      440      445
276 Ile Ser Thr Val Glu Leu Lys Val Val Gln Gly Glu Pro Ser Leu Lys
277      450      455      460
279 Val Pro Lys Asn Val Thr Ala Trp Leu Gly Glu Pro Leu Lys Leu Ser
280 465      470      475      480
282 Cys His Phe Pro Cys Lys Phe Tyr Ser Phe Glu Lys Tyr Trp Cys Lys
283      485      490      495
285 Trp Ser Asn Arg Gly Cys Ser Ala Leu Pro Thr Gln Asn Asp Gly Pro

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```

286          500          505          510
288 Ser Gln Ala Phe Val Ser Cys Asp Gln Asn Ser Gln Val Val Ser Leu
289          515          520          525
291 Asn Leu Asp Thr Val Thr Lys Glu Asp Glu Gly Trp Tyr Trp Cys Gly
292          530          535          540
294 Val Lys Glu Gly Pro Arg Tyr Gly Glu Thr Ala Ala Val Tyr Val Ala
295 545          550          555          560
297 Val Glu Ser Arg Val Lys Gly Ser Gln Gly Ala Lys Gln Val Lys Ala
298          565          570          575
300 Ala Pro Ala Gly Ala Ala Ile Gln Ser Arg Ala Gly Glu Ile Gln Asn
301          580          585          590
303 Lys Ala Leu Leu Asp Pro Ser Phe Phe Ala Lys Glu Ser Val Lys Asp
304          595          600          605
306 Ala Ala Gly Gly Pro Gly Ala Pro Ala Asp Pro Gly Arg Pro Thr Gly
307          610          615          620
309 Tyr Ser Gly Ser Ser Lys Ala Leu Val Ser Thr Leu Val Pro Leu Ala
310 625          630          635          640
312 Leu Val Leu Val Ala Gly Val Val Ala Ile Gly Val Val Arg Ala Arg
313          645          650          655
315 His Arg Lys Asn Val Asp Arg Ile Ser Ile Arg Ser Tyr Arg Thr Asp
316          660          665          670
318 Ile Ser Met Ser Asp Phe Glu Asn Ser Arg Asp Phe Glu Gly Arg Asp
319          675          680          685
321 Asn Met Gly Ala Ser Pro Glu Ala Gln Glu Thr Ser Leu Gly Gly Lys
322          690          695          700
324 Asp Glu Phe Ala Thr Thr Thr Glu Asp Thr Val Glu Ser Lys Glu Pro
325 705          710          715          720
327 Lys Lys Ala Lys Arg Ser Ser Lys Glu Glu Ala Asp Glu Ala Phe Thr
328          725          730          735
330 Thr Phe Leu Leu Gln Ala Lys Asn Leu Ala Ser Ala Ala Thr Gln Asn
331          740          745          750
333 Gly Pro Thr Glu Ala
334          755
337 <210> SEQ ID NO: 3
338 <211> LENGTH: 769
339 <212> TYPE: PRT
340 <213> ORGANISM: Rattus sp.
342 <220> FEATURE:
343 <223> OTHER INFORMATION: rat polymeric immunoglobulin receptor (pIgR)
345 <400> SEQUENCE: 3
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347 1          5          10          15
349 Ser Thr Gln Ser Pro Ile Phe Gly Pro Gln Asp Val Ser Ser Ile Glu
350          20          25          30
352 Gly Asn Ser Val Ser Ile Thr Cys Tyr Tyr Pro Asp Thr Ser Val Asn
353          35          40          45
355 Arg His Thr Arg Lys Tyr Trp Cys Arg Gln Gly Ala Asn Gly Tyr Cys
356          50          55          60
358 Ala Thr Leu Ile Ser Ser Asn Gly Tyr Leu Ser Lys Glu Tyr Ser Gly

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